Amendments to the Specification

Please insert the Substitute Sequence Listing that is appended hereto at the end of the specification.

Please replace the paragraph starting on page 4, line 1 with the following paragraph:

It is therefore an object of the invention to provide an isolated nucleic acid molecule encoding the transcription factor *Hahb-4*, a functionally active fragment or variant thereof, having the nucleic acid sequence of SEQ ID NO:1 ~~SEQ ID N° 1~~ or a fragment thereof, wherein the nucleic acid molecule is derived from *Helianthus annuus*, and it may be an mRNA or the cDNA of SEQ ID NO:2 ~~SEQ ID N° 2~~, wherein the molecule is capable of binding to a 5'-CAAT(A/T)ATTG-3' DNA sequence (SEQ ID NO:23) or to a dehydration transcription regulating region of plant species.

Please replace the paragraph starting on page 9, line 6 with the following paragraph:

It is a further object of the present invention to provide a transgenic plant stably transformed with at least one of the above mentioned constructs, wherein the protein of interest is the transcription factor *Hahb-4*, having the nucleic acid sequence selected from the group comprising SEQ ID NO:1, SEQ ID NO:2 ~~SEQ ID N° 1, SEQ ID N° 2~~ and fragments thereof, and wherein the plant is selected from the group comprising monocot and dicot plants and said plant is environmental stress tolerant to situations like drought, high salinity, high osmotic pressure and others, and preferably the plant is

resistant and tolerant to water deficit. Most preferably, the plant is water stress tolerant by binding the transcription factor *Hahb-4* or a functionally active fragment or variant thereof to a dehydration transcription regulating region of the plant and the dehydration transcription regulating region of the plant is a 5'-CAAT(A/T)ATTG-3' DNA sequence (SEQ ID NO:23).

Please replace the paragraph starting on page 10, line 4 with the following paragraph:

Figure 1 shows the genomic sequence encoding sunflower *Hahb-4* of the invention. The deduced protein sequence of the open reading frame (SEQ ID NO:24) is indicated below the nucleotide sequence (SEQ ID NO:1). The homeodomain is shown in bold; leucines from the leucine zipper are shown in bold and underlined. The lower part of the Figure shows an alignment of the Hd-Zip domain of *Hahb-4* (SEQ ID NO:29) with those of *Athb-1* (SEQ ID NO: 25), -6 (SEQ ID NO: 26), -7 (SEQ ID NO:27) and -12 (SEQ ID NO:28). Shaded boxes indicate identical amino acids.

Please replace the paragraph starting on page 14, line 12 with the following paragraph:

Figure 18 shows the sequence of nucleotides of the promoter region of *Hahb-4* gene (SEQ ID NO:3), remarking the sequences corresponding to the TATA box, the element responding to water stress/low temperatures, ABRE regions and the sequences indicating the recognizing sites of Myb and Myc.

Please replace the paragraph starting at page 15, line 14 with the following paragraph:

Figure 23 shows a scheme of *Hahb-4* gene structure. At the top: large allele ~~allele~~, at the bottom: small allele ~~allele~~. The oligonucleotides employed for the isolation of the promoting region and for the construction of recombinant plasmids and used in plant transformation are indicated.

Please replace the paragraph beginning on page 47, line 20 of the specification with the following paragraph:

The PCR reactions in the first step were made by using as a template the DNA from the recycling of the fragments digested with *Sau*IIIA, with oligonucleotides IPCR0/IPCR1 (SEQ ID NO:12/SEQ ID NO:15) ~~(SEQ ID N° 12/SEQ ID N°15)~~ and in the case of the DNA digested with *Hin*dIII, the employed oligonucleotides were IPCR2/IPCR3 (SEQ ID NO:16/SEQ ID NO:17) ~~(SEQ ID N° 16/SEQ ID N° 17)~~. The obtained fragments were cloned in *pGEM®-T easy* vector (Promega), according to the protocol suggested by the manufacturer. Once the cloning was verified, the corresponding sequence was determined and the oligonucleotides necessary for the next step were designed. The sequence and location of the oligonucleotides used in the next cloning steps are shown in Figure 23:

IPCR0 [5′-GGCGGATCCCCTGGTGGTTGTTTCTGTTG-3′] (SEQ ID NO:12)
IPCR1 [5′-GCCGAATTCAGATTGAGCAAGAGTATAAC-3′] (SEQ ID NO:15)
IPCR2 [5′-ACCTTTATAAAGACCACTC-3′] (SEQ ID NO:16)
IPCR3 [5′-ACGCAATGGTGAGTTGTAC-3′] (SEQ ID NO:17)
IPCR4 [5'-GCGAAGCTTGATGCGAACGAGTGGTTTA] (SEQ ID NO:4)
IPCR5 [5′-ATTTCGCAAGTAGTCCATT-3′] (SEQ ID NO:9)
IPCR6 [5′-CCCAAGCTTAACCTAAGTCCGCCTTTG-3′] (SEQ ID NO:7)
IPCR7 [5'-GGCAAGCTTATCTCAACCGAAAGTGAC-3] (SEQ ID NO:8)